

SEQUENCE LISTING

<110> Boehringer Ingelheim Pharma KG

<120> Methods for identifying substances for treating
inflammatory conditions

<130> 1/1178

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<150> US 60/257,878

<151> 2000-12-22

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<170> PatentIn Ver. 2.1

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Cys Gly Leu Leu Ala Glu Arg Leu Arg Ile Ser Pro Asp Arg Val Tyr
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20

25

30

Val Arg Arg Gly Gln Pro Phe Trp Leu Thr Leu His Phe Glu Gly Arg
35 40 45

Asn Tyr Gln Ala Ser Val Asp Ser Leu Thr Phe Ser Val Val Thr Gly
50 55 60

Pro Ala Pro Ser Gln Glu Ala Gly Thr Lys Ala Arg Phe Pro Leu Arg
65 70 75 80

Asp Ala Val Glu Glu Gly Asp Trp Thr Ala Thr Val Val Asp Gln Gln
85 90 95

Asp Cys Thr Leu Ser Leu Gln Leu Thr Thr Pro Ala Asn Ala Pro Ile
100 105 110

Gly Leu Tyr Arg Leu Ser Leu Glu Ala Ser Thr Gly Tyr Gln Gly Ser
115 120 125

Ser Phe Val Leu Gly His Phe Ile Leu Leu Phe Asn Ala Trp Cys Pro
130 135 140

Ala Asp Ala Val Tyr Leu Asp Ser Glu Glu Glu Arg Gln Glu Tyr Val
145 150 155 160

Leu Thr Gln Gln Gly Phe Ile Tyr Gln Gly Ser Ala Lys Phe Ile Lys
165 170 175

Asn Ile Pro Trp Asn Phe Gly Gln Phe Gln Asp Gly Ile Leu Asp Ile
180 185 190

Cys Leu Ile Leu Leu Asp Val Asn Pro Lys Phe Leu Lys Asn Ala Gly
195 200 205

Arg Asp Cys Ser Arg Arg Ser Ser Pro Val Tyr Val Gly Arg Val Gly
210 215 220

Ser Gly Met Val Asn Cys Asn Asp Asp Gln Gly Val Leu Leu Gly Arg
225 230 235 240

Trp Asp Asn Asn Tyr Gly Asp Gly Val Ser Pro Met Ser Trp Ile Gly
 245 250 255

Ser Val Asp Ile Leu Arg Arg Trp Lys Asn His Gly Cys Gln Arg Val
 260 265 270

Lys Tyr Gly Gln Cys Trp Val Phe Ala Ala Val Ala Cys Thr Val Leu
 275 280 285

Arg Cys Leu Gly Ile Pro Thr Arg Val Val Thr Asn Tyr Asn Ser Ala
 290 295 300

His Asp Gln Asn Ser Asn Leu Leu Ile Glu Tyr Phe Arg Asn Glu Phe
 305 310 315 320

Gly Glu Ile Gln Gly Asp Lys Ser Glu Met Ile Trp Asn Phe His Cys
 325 330 335

Trp Val Glu Ser Trp Met Thr Arg Pro Asp Leu Gln Pro Gly Tyr Glu
 340 345 350

Gly Trp Gln Ala Leu Asp Pro Thr Pro Gln Glu Lys Ser Glu Gly Thr
 355 360 365

Tyr Cys Cys Gly Pro Val Pro Val Arg Ala Ile Lys Glu Gly Asp Leu
 370 375 380

Ser Thr Lys Tyr Asp Ala Pro Phe Val Phe Ala Glu Val Asn Ala Asp
 385 390 395 400

Val Val Asp Trp Ile Gln Gln Asp Asp Gly Ser Val His Lys Ser Ile
 405 410 415

Asn Arg Ser Leu Ile Val Gly Leu Lys Ile Ser Thr Lys Ser Val Gly
 420 425 430

Arg Asp Glu Arg Glu Asp Ile Thr His Thr Tyr Lys Tyr Pro Glu Gly

435

440

445

Ser Ser Glu Glu Arg Glu Ala Phe Thr Arg Ala Asn His Leu Asn Lys
450 455 460

Leu Ala Glu Lys Glu Glu Thr Gly Met Ala Met Arg Ile Arg Val Gly
465 470 475 480

Gln Ser Met Asn Met Gly Ser Asp Phe Asp Val Phe Ala His Ile Thr
485 490 495

Asn Asn Thr Ala Glu Glu Tyr Val Cys Arg Leu Leu Leu Cys Ala Arg
500 505 510

Thr Val Ser Tyr Asn Gly Ile Leu Gly Pro Glu Cys Gly Thr Lys Tyr
515 520 525

Leu Leu Asn Leu Thr Leu Glu Pro Phe Ser Glu Lys Ser Val Pro Leu
530 535 540

Cys Ile Leu Tyr Glu Lys Tyr Arg Asp Cys Leu Thr Glu Ser Asn Leu
545 550 555 560

Ile Lys Val Arg Ala Leu Leu Val Glu Pro Val Ile Asn Ser Tyr Leu
565 570 575

Leu Ala Glu Arg Asp Leu Tyr Leu Glu Asn Pro Glu Ile Lys Ile Arg
580 585 590

Ile Leu Gly Glu Pro Lys Gln Lys Arg Lys Leu Val Ala Glu Val Ser
595 600 605

Leu Gln Asn Pro Leu Pro Val Ala Leu Glu Gly Cys Thr Phe Thr Val
610 615 620

Glu Gly Ala Gly Leu Thr Glu Glu Gln Lys Thr Val Glu Ile Pro Asp
625 630 635 640

Pro Val Glu Ala Gly Glu Glu Val Lys Val Arg Met Asp Leu Val Pro

645

650

655

Leu His Met Gly Leu His Lys Leu Val Val Asn Phe Glu Ser Asp Lys

660

665

670

Leu Lys Ala Val Lys Gly Phe Arg Asn Val Ile Ile Gly Pro Ala

675

680

685

<210> 11

<211> 1470

<212> DNA

<213> Homo sapiens

<400> 11

gacgggcacc cgttgccagc tctagccttt aaattcccg ctcgggggacc tccacgcacc 60
gcggctagcg ccgacaacca gctagcgtgc aaggcgccgc ggctcagcgc gtaccggcgg 120
gtttcgaaac cgcagtcctc cggcgacccc gaactccgct cgggagcctc agccccctgg 180
aaagtgatcc cggcatcgga gagccaagat gccggcccac ttgctgcagg acgatatctc 240
tagctcctat accaccacca ccaccattac agcgccctct ccaggggtcc tgcagaatgg 300
aggagataag ttggagacga tgcccctcta cttggaagac gacattcgcc ctgatataaa 360
agatgatata tatgacccca cctacaagga taagggaaggc ccaagcccca aggttgataa 420
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tgccctgggc ataacagcag gagctcatcg tctgtggagc caccgctctt acaaagctcg 600
gctgcccta cggctcttct tgatcattgc caacacaatg gcattccaga atgatgtcta 660
tgaatgggct cgtgaccacc gtgcccacca caagttttca gaaacacatg ctgacctcta 720
taattcccca cgtggctttt tcttctctca cgtgggttgg ctgcttgtgc gcaaacaccc 780
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tctgacctat gaccggaaga aagtctccaa ggccgccatc ttggccagga ttaaaagaac 1260
cggagatgga aactacaaga gtggctgagt ttggggtccc tcaggttctct ttttcaaaaa 1320

ccagccaggc agaggtttta atgtctgttt attaactact gaataatgct accaggatgc 1380
 taaagatgat gatgttaacc cattccagta cagtattctt ttaaaattca aaagtattga 1440
 aagccaaaaa aaaaaaaaaa aaaaaaaaaa 1470

<210> 12

<211> 359

<212> PRT

<213> Homo sapiens

<400> 12

Met Pro Ala His Leu Leu Gln Asp Asp Ile Ser Ser Ser Tyr Thr Thr

1 5 10 15

Thr Thr Thr Ile Thr Ala Pro Pro Pro Gly Val Leu Gln Asn Gly Gly

20 25 30

Asp Lys Leu Glu Thr Met Pro Leu Tyr Leu Glu Asp Asp Ile Arg Pro

35 40 45

Asp Ile Lys Asp Asp Ile Tyr Asp Pro Thr Tyr Lys Asp Lys Glu Gly

50 55 60

Pro Ser Pro Lys Val Glu Tyr Val Trp Arg Asn Ile Ile Leu Met Ser

65 70 75 80

Leu Leu His Leu Gly Ala Leu Tyr Gly Ile Thr Leu Ile Pro Thr Cys

85 90 95

Lys Phe Tyr Thr Trp Leu Trp Gly Val Phe Tyr Tyr Phe Val Ser Ala

100 105 110

Leu Gly Ile Thr Ala Gly Ala His Arg Leu Trp Ser His Arg Ser Tyr

115 120 125

Lys Ala Arg Leu Pro Leu Arg Leu Phe Leu Ile Ile Ala Asn Thr Met

130 135 140

Ala Phe Gln Asn Asp Val Tyr Glu Trp Ala Arg Asp His Arg Ala His
145 150 155 160

His Lys Phe Ser Glu Thr His Ala Asp Pro His Asn Ser Arg Arg Gly
165 170 175

Phe Phe Phe Ser His Val Gly Trp Leu Leu Val Arg Lys His Pro Ala
180 185 190

Val Lys Glu Lys Gly Ser Thr Leu Asp Leu Ser Asp Leu Glu Ala Glu
195 200 205

Lys Leu Val Met Phe Gln Arg Arg Tyr Tyr Lys Pro Gly Leu Leu Met
210 215 220

Met Cys Phe Ile Leu Pro Thr Leu Val Pro Trp Tyr Phe Trp Gly Glu
225 230 235 240

Thr Phe Gln Asn Ser Val Phe Val Ala Thr Phe Leu Arg Tyr Ala Val
245 250 255

Val Leu Asn Ala Thr Trp Leu Val Asn Ser Ala Ala His Leu Phe Gly
260 265 270

Tyr Arg Pro Tyr Asp Lys Asn Ile Ser Pro Arg Glu Asn Ile Leu Val
275 280 285

Ser Leu Gly Ala Val Gly Glu Gly Phe His Asn Tyr His His Ser Phe
290 295 300

Pro Tyr Asp Tyr Ser Ala Ser Glu Tyr Arg Trp His Ile Asn Phe Asn
305 310 315 320

Thr Phe Phe Ile Asp Trp Met Ala Ala Leu Gly Leu Thr Tyr Asp Arg
325 330 335

Lys Lys Val Ser Lys Ala Ala Ile Leu Ala Arg Ile Lys Arg Thr Gly

Asp Gly Asn Tyr Lys Ser Gly

355

<210> 13

<211> 1637

<212> DNA

<213> Homo sapiens

<400> 13

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 cgcagggccct gccgcgccct tcggtcccca cccccctcg cctctctctc tccccacatt 180
 cctctcgctt cccgcgcccc cgcaccgggc gccaccacct tcctctctct gcggggagcgt 240
 tgtccgtgtt ggcgcccgca gcgggcccgg cggtccggc gggccggggg atggcgctgc 300
 tggacctggc cttggaggga atggcgctct cggggttcgt cctctctctg gtgctgtggc 360
 tgatgcattt catggctatc atctacaccc gattacacct caacaagaag gcaactgaca 420
 aacagcctta tagcaagctc ccaggtgtct ctctcttgaa accactgaaa ggggtagatc 480
 ctaacttaat caacaacctg gaaacattct ttgaattgga ttatcccaaa tatgaagtgc 540
 tcctttgtgt acaagatcat gatgatccag ccattgatgt atgtaagaag cttcttgga 600
 aatatccaaa tgttgatgct agattgttta tagtggttaa aaaagtggc attaatccta 660
 aaattaataa tttaatgcca ggatatgaag ttgcaaagta tgatctata tggatttgtg 720
 atagtggaa aagagtaatt ccagatacgc ttaactgacat ggtgaatcaa atgacagaaa 780
 aagtaggctt ggttcacggg ctgccttacg tagcagacag acagggcttt gctgccacct 840
 tagagcaggt atattttgga acttcacatc caagatacta tatctctgcc aatgtaactg 900
 gtttcaaatg tgtgacagga atgtcttgtt taatgagaaa agatgtgttg gatcaagcag 960
 gaggacttat agcttttgct cagtcatttg ccgaagatta ctttatggcc aaagcgatag 1020
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 attcaatttc tcagtttcaa tcagaatga tcaggtggac caaactaga attaacatgc 1140
 ttctgtctac aataatttgt gagccaatct cagaatgctt tgttgccagt ttaattattg 1200
 gatgggcagc ccaccatgtg ttcagatggg atattatggt attttctatg tgcattggc 1260
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 gtgggggtac agcagaggaa atcctagatg tataactaca gcttctgtac tgtatataaa 1500
 ggaaaaaaga gaagtattat aaattatggt tatataaatg cttttaaaaa tctacctctc 1560

gtagttttat cacatgtatg ttttggtatc tgttctttaa tttatttttg catggcactt 1620
gcactctgtga aaaaaaa 1637

<210> 14
<211> 394
<212> PRT
<213> Homo sapiens

<400> 14
Met Ala Leu Leu Asp Leu Ala Leu Glu Gly Met Ala Val Phe Gly Phe
1 5 10 15
Val Leu Phe Leu Val Leu Trp Leu Met His Phe Met Ala Ile Ile Tyr
20 25 30
Thr Arg Leu His Leu Asn Lys Lys Ala Thr Asp Lys Gln Pro Tyr Ser
35 40 45
Lys Leu Pro Gly Val Ser Leu Leu Lys Pro Leu Lys Gly Val Asp Pro
50 55 60
Asn Leu Ile Asn Asn Leu Glu Thr Phe Phe Glu Leu Asp Tyr Pro Lys
65 70 75 80
Tyr Glu Val Leu Leu Cys Val Gln Asp His Asp Asp Pro Ala Ile Asp
85 90 95
Val Cys Lys Lys Leu Leu Gly Lys Tyr Pro Asn Val Asp Ala Arg Leu
100 105 110
Phe Ile Gly Gly Lys Lys Val Gly Ile Asn Pro Lys Ile Asn Asn Leu
115 120 125
Met Pro Gly Tyr Glu Val Ala Lys Tyr Asp Leu Ile Trp Ile Cys Asp
130 135 140

Ser Gly Ile Arg Val Ile Pro Asp Thr Leu Thr Asp Met Val Asn Gln
145 150 155 160

Met Thr Glu Lys Val Gly Leu Val His Gly Leu Pro Tyr Val Ala Asp
165 170 175

Arg Gln Gly Phe Ala Ala Thr Leu Glu Gln Val Tyr Phe Gly Thr Ser
180 185 190

His Pro Arg Tyr Tyr Ile Ser Ala Asn Val Thr Gly Phe Lys Cys Val
195 200 205

Thr Gly Met Ser Cys Leu Met Arg Lys Asp Val Leu Asp Gln Ala Gly
210 215 220

Gly Leu Ile Ala Phe Ala Gln Tyr Ile Ala Glu Asp Tyr Phe Met Ala
225 230 235 240

Lys Ala Ile Ala Asp Arg Gly Trp Arg Phe Ala Met Ser Thr Gln Val
245 250 255

Ala Met Gln Asn Ser Gly Ser Tyr Ser Ile Ser Gln Phe Gln Ser Arg
260 265 270

Met Ile Arg Trp Thr Lys Leu Arg Ile Asn Met Leu Pro Ala Thr Ile
275 280 285

Ile Cys Glu Pro Ile Ser Glu Cys Phe Val Ala Ser Leu Ile Ile Gly
290 295 300

Trp Ala Ala His His Val Phe Arg Trp Asp Ile Met Val Phe Phe Met
305 310 315 320

Cys His Cys Leu Ala Trp Phe Ile Phe Asp Tyr Ile Gln Leu Arg Gly
325 330 335

Val Gln Gly Gly Thr Leu Cys Phe Ser Lys Leu Asp Tyr Ala Val Ala
340 345 350

Trp Phe Ile Arg Glu Ser Met Thr Ile Tyr Ile Phe Leu Ser Ala Leu
355 360 365

Trp Asp Pro Thr Ile Ser Trp Arg Thr Gly Arg Tyr Arg Leu Arg Cys
370 375 380

Gly Gly Thr Ala Glu Glu Ile Leu Asp Val
385 390

<210> 15

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 15

ggccagtgaa ttgtaatacg actcactata gggaggcggt tttttttttt tttttttttt

60

ttt

63

<210> 16

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 16

gtcgtcaaga tgctaccgtt cagga

25

<210> 17
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
ggggacaagt ttgtacaaaa aagcaggcta tgccgatgtt catcgtaaac a
51

<210> 18
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
ggggaccact ttgtacaaga aagctggggt taggcgaagg tggagtgtt
50

<210> 19
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19

aaggattcgg gaatgggctg tcagaccaga ct

32

<210> 20

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 20

ttaagctttc atcttttctt tttctgttg c

31